KB #4

PCT09

RAW SEQUENCE LISTING   DATE: 09/27/2001
PATENT APPLICATION: US/09/831,656   TIME: 11:59:29

Input Set : A:\5753prj.ST25.txt
Output Set: N:\CRF3\09272001\I831656.raw

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  3 <110> APPLICANT: Novozymes A/S
  4        Nielsen, Jack Bech
  5        Kjaerulff, Soren
  7 <120> TITLE OF INVENTION: Transgenic Plant Expressing Maltogenic Alpha-Amylase
  9 <130> FILE REFERENCE: 5753.204-US
 11 <140> CURRENT APPLICATION NUMBER: 09/831,656
C--> 12 <141> CURRENT FILING DATE: 2001-08-23
 14 <150> PRIOR APPLICATION NUMBER: PCT/DK99/00624
 15 <151> PRIOR FILING DATE: 1999-11-12
 17 <160> NUMBER OF SEQ ID NOS: 4
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 2160
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Bacillus sp.
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 31 ggggacgtga tttaccagat tatcattgac cggttttacg atggggacac gacgaacaac      180
 33 aatcctgcca aaagttatgg actttacgat ccgaccaaat cgaagtggaa aatgtattgg      240
 35 ggcggggatc tggagggggt tcgtcaaaaa cttccttatc ttaaacagct gggcgtaacg      300
 37 acaatctggt tgtccccggt tttggacaat ctggatacac tggcgggcac cgataacacg      360
 39 ggctatcacg gatactggac gcgcgatttt aaacagattg aggaacattt cgggaattgg      420
 41 accacatttg acacgttggt caatgatgct caccaaaacg gaatcaaggt gattgtcgac      480
 43 tttgtgccca atcattcgac tccttttaag gcaaacgatt ccacctttgc ggaaggcggc      540
 45 gccctctaca caatggaac  ctatatgggc aattattttg atgacgcaac aaaagggtac      600
 47 ttccaccata tggggacat  cagcaactgg gacgaccggt acgaggcgca atggaaaaac      660
 49 ttcacggatc cagccggttt ctcgcttgcc gatttgtcgc aggaaaatgg cacgattgct      720
 51 caatacctga ccgatgcggc ggttcaattg gtagcacatg gagcggatgg tttgcggatt      780
 53 gatgcggtga agcatttaa  ttcggggttc tccaaatcgt tggccgataa actgtaccaa      840
 55 aagaaagaca ttttcctggt gggggaatgg tacggagatg accccggaac agccaatcat      900
 57 ctggaaaagg tccggtacgc caacaacagc ggtgtcaatg tgctggattt tgatctcaac      960
 59 acggtgattc gaaatgtgtt cggcacattt acgcaaacga tgtacgatct taacaatatg     1020
 61 gtgaaccaaa cggggaacga gtacaaatac aagaaaatc  taatcacatt tatcgataac     1080
 63 catgatatgt caagatttct ttcggtaaat tcgaacaagg cgaatttgca ccaggcgctt     1140
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 67 gcaggcggca tgacccgta  caaccggggg atgatgccgg cgtttgatac gacaaccacc     1260
 69 gcctttaaag aggtgtcaac tctggcgggg ttgcgcagga caatgcggc  gatccagtac     1320
 71 ggcaccacca cccagcgttg gatcaacaat gatgtttaca tttatgaacg gaaatttttc     1380
 73 aacgatgtcg tgttggtggc catcaatcga aacacgcaat cctcctattc gatttccggt     1440
 75 ttgcagacgg ccttgccaaa tggcagctat gcggattatc tgtcagggct gttggggggg     1500
 77 aacgggattt ccgtttccaa tggaagtgtc gcttcgttca cgcttgcgcc tggagccgtg     1560
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 83 accgtgacat ttggcggagt gacagcgact gtgaaatcct ggacatccaa tcggattgaa     1740
 85 gtgtacgttc ccaacatggc cgccgggctg accgatgtga aagtcaccgc gggtggagtt     1800
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 93 ctcgcgccca attatccgga ttggtttttat gtattcagcg ttccagcagg aaagacgatt   2040
 95 caattcaagt tcttcatcaa gcgtgcggat ggaacgattc aatgggagaa tggttcgaac   2100
 97 cacgtggcca caactcccac gggtgcaacc ggtaacatta ctgttacgtg gcaaaactag   2160
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101 <211> LENGTH: 719
102 <212> TYPE: PRT
103 <213> ORGANISM: Bacillus sp
105 <400> SEQUENCE: 2
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112             20                  25                  30
115 Ala Ser Ser Ser Ala Ser Val Lys Gly Asp Val Ile Tyr Gln Ile Ile
116         35                  40                  45
119 Ile Asp Arg Phe Tyr Asp Gly Asp Thr Thr Asn Asn Asn Pro Ala Lys
120     50                  55                  60
123 Ser Tyr Gly Leu Tyr Asp Pro Thr Lys Ser Lys Trp Lys Met Tyr Trp
124 65                  70                  75                  80
127 Gly Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln
128             85                  90                  95
131 Leu Gly Val Thr Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp
132             100                 105                 110
135 Thr Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg
136         115                 120                 125
139 Asp Phe Lys Gln Ile Glu Glu His Phe Gly Asn Trp Thr Thr Phe Asp
140     130                 135                 140
143 Thr Leu Val Asn Asp Ala His Gln Asn Gly Ile Lys Val Ile Val Asp
144 145                 150                 155                 160
147 Phe Val Pro Asn His Ser Thr Pro Phe Lys Ala Asn Asp Ser Thr Phe
148             165                 170                 175
151 Ala Glu Gly Gly Ala Leu Tyr Asn Asn Gly Thr Tyr Met Gly Asn Tyr
152             180                 185                 190
155 Phe Asp Asp Ala Thr Lys Gly Tyr Phe His His Asn Gly Asp Ile Ser
156         195                 200                 205
159 Asn Trp Asp Asp Arg Tyr Glu Ala Gln Trp Lys Asn Phe Thr Asp Pro
160     210                 215                 220
163 Ala Gly Phe Ser Leu Ala Asp Leu Ser Gln Glu Asn Gly Thr Ile Ala
164 225                 230                 235                 240
167 Gln Tyr Leu Thr Asp Ala Ala Val Gln Leu Val Ala His Gly Ala Asp
168             245                 250                 255
171 Gly Leu Arg Ile Asp Ala Val Lys His Phe Asn Ser Gly Phe Ser Lys
172             260                 265                 270
175 Ser Leu Ala Asp Lys Leu Tyr Gln Lys Lys Asp Ile Phe Leu Val Gly
176         275                 280                 285
179 Glu Trp Tyr Gly Asp Asp Pro Gly Thr Ala Asn His Leu Glu Lys Val
180     290                 295                 300
183 Arg Tyr Ala Asn Asn Ser Gly Val Asn Val Leu Asp Phe Asp Leu Asn
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184 305                    310                   315                     320
187 Thr Val Ile Arg Asn Val Phe Gly Thr Phe Thr Gln Thr Met Tyr Asp
188             325                   330                   335
191 Leu Asn Asn Met Val Asn Gln Thr Gly Asn Glu Tyr Lys Tyr Lys Glu
192             340                   345                   350
195 Asn Leu Ile Thr Phe Ile Asp Asn His Asp Met Ser Arg Phe Leu Ser
196             355                   360                   365
199 Val Asn Ser Asn Lys Ala Asn Leu His Gln Ala Leu Ala Phe Ile Leu
200     370                   375                   380
203 Thr Ser Arg Gly Thr Pro Ser Ile Tyr Tyr Gly Thr Glu Gln Tyr Met
204 385                   390                   395                   400
207 Ala Gly Gly Asn Asp Pro Tyr Asn Arg Gly Met Met Pro Ala Phe Asp
208             405                   410                   415
211 Thr Thr Thr Thr Ala Phe Lys Glu Val Ser Thr Leu Ala Gly Leu Arg
212             420                   425                   430
215 Arg Asn Asn Ala Ala Ile Gln Tyr Gly Thr Thr Thr Gln Arg Trp Ile
216             435                   440                   445
219 Asn Asn Asp Val Tyr Ile Tyr Glu Arg Lys Phe Phe Asn Asp Val Val
220     450                   455                   460
223 Leu Val Ala Ile Asn Arg Asn Thr Gln Ser Ser Tyr Ser Ile Ser Gly
224 465                   470                   475                   480
227 Leu Gln Thr Ala Leu Pro Asn Gly Ser Tyr Ala Asp Tyr Leu Ser Gly
228             485                   490                   495
231 Leu Leu Gly Gly Asn Gly Ile Ser Val Ser Asn Gly Ser Val Ala Ser
232             500                   505                   510
235 Phe Thr Leu Ala Pro Gly Ala Val Ser Val Trp Gln Tyr Ser Thr Ser
236             515                   520                   525
239 Ala Ser Ala Pro Gln Ile Gly Ser Val Ala Pro Asn Met Gly Ile Pro
240     530                   535                   540
243 Gly Asn Val Val Thr Ile Asp Gly Lys Gly Phe Gly Thr Thr Gln Gly
244 545                   550                   555                   560
247 Thr Val Thr Phe Gly Gly Val Thr Ala Thr Val Lys Ser Trp Thr Ser
248             565                   570                   575
251 Asn Arg Ile Glu Val Tyr Val Pro Asn Met Ala Ala Gly Leu Thr Asp
252             580                   585                   590
255 Val Lys Val Thr Ala Gly Gly Val Ser Ser Asn Leu Tyr Ser Tyr Asn
256             595                   600                   605
259 Ile Leu Ser Gly Thr Gln Thr Ser Val Val Phe Thr Val Lys Ser Ala
260     610                   615                   620
263 Pro Pro Thr Asn Leu Gly Asp Lys Ile Tyr Leu Thr Gly Asn Ile Pro
264 625                   630                   635                   640
267 Glu Leu Gly Asn Trp Ser Thr Asp Thr Ser Gly Ala Val Asn Asn Ala
268             645                   650                   655
271 Gln Gly Pro Leu Leu Ala Pro Asn Tyr Pro Asp Trp Phe Tyr Val Phe
272             660                   665                   670
275 Ser Val Pro Ala Gly Lys Thr Ile Gln Phe Lys Phe Phe Ile Lys Arg
276         675                   680                   685
279 Ala Asp Gly Thr Ile Gln Trp Glu Asn Gly Ser Asn His Val Ala Thr
280     690                   695                   700
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288 <211> LENGTH: 33
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: FNP 110
295 <400> SEQUENCE: 3
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300 <211> LENGTH: 25
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: RNP 110
307 <400> SEQUENCE: 4
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VERIFICATION SUMMARY
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date